REMARKS

Amendments to the specification.

Applicants believe no new matter is added by this amendment.

The Substitute Sequence Listing is being submitted in response to the Examiner's request to amend the specification to refer to corresponding SEQ ID NOs, which necessitates adding the sequences that appear in the specification to the Sequence Listing.

Support for the amendment to add sequences to the Sequence Listing can be found in Figure 6 and in the specification at the specific pages and lines noted in the "Amendments to the Specification" noted above. The substitute sequence listing thus contains no new matter. Support for the amendment to add the file creation date to the paragraph on page 8, line 26 is supported by the file creation date on the CD-ROMs filed with the present application.

Support for the amendment to the paragraph beginning on page 9, line 21, to amend the phrase "indicated by the line that spans Figures 6B through 6D" to "indicated by the line that spans Figures 6B through 6C" is supported by Figure 6C as filed.

Amendments to the claims.

Claims 7-9, 14 and 16-35 are canceled. Claims 1, 5, 6, 10, 12, and 13 are currently amended. New claims 36-28 have been added.

Support for amendments to the claims may be found in the claims as a whole.

Support for "specific" hybridization may be found, for example, on page 45, lines 4, 9 and 28, and on page 46 at line 14.

Support for the wash conditions of --1x SSC, 1% SDS at 60° C for 45-60 minutes for each wash step-- may be found in the present specification on, for example, page 82, line 17.

Support for the wash conditions of --0.5X SSC, 0.1% SDS at 65° C of 10 - 30 minutes for each step-- may be found in the present specification on, for example, page 46, lines 24-25.

Support for a --transgenic seed produced by the transgenic plant of Claim 1-- found in new claim 36 may be found, for example, on page 10, lines 5-8, Figure 8B, page 84, lines 24 to page 85, line 11, page 85, line 34, and page 92, lines 6-12.

Response to specific items in the Office action

Item 4. Priority

Independent claims 1 and 12 have been amended such that the recombinant polynucleotide comprised within the transgenic plants of the invention specifically hybridizes to the complement of the sequence set forth in SEQ ID NO: 3 under stringent conditions comprising two wash steps of 1x SSC, 1% SDS at 60° C for 45-60 minutes for each wash step. Support for both SEQ ID NO: 3 and hybridization

language may be found in the present application, as noted above, and also in priority applications 60/125,814, filed March 23, 1999 (e.g., sequence "G482" in "Family 13. CAAT Binding Protein...", and on page 47, lines 1-2 and page 63, lines 25-31) , and 60/166,228, filed November 17, 1999 (e.g., see the pages for "Summary of Overexpressor G482, Family CAAT", and page 20, lines 10-11). The former application teaches how to prepare transgenic plants, and the latter application discloses osmotic stress-tolerant transgenic plants overexpressing G481 (present SEQ ID NO: 2) and salt-tolerant transgenic plants overexpressing G482 (presently SEQ ID NO: 4).

Accordingly, Applicants believe these and subsequent priority applications disclose the present sequences, transgenic plants, and methods for determining abiotic stress tolerance.

Item 6. Drawings.

In response to the Examiner's objection, Figures 6A-6F have been amended to include SEQ ID NOs for the sequences provided in the figure.

Item 7. Specification.

In response to the Examiners request to cancel the amendment of the first paragraph, said amendment has been canceled. The paragraph is now amended as noted above, and lists only those applications originally presented in the application as filed, said priority applications having been incorporated by reference. Support for the amendment to add " --is a continuation-in-part of-- U.S. Application No. 10/412,699" is provided by the Application Data Sheet filed with the present application.

Item 8. Specification.

Table 6 has been amended and the top row is now visible.

In response to the Examiner's objection, the paragraphs referred to in the objection have been amended to include SEQ ID NOs for the sequences provided in the specification.

The sequences provided on page 23, line 21 (PKK/RPAGRxKFxETRHP and DSAWR) are art-known sequences (provided in the Jaglo reference cited on page 25, lines 6 and 13; the sequences appear in column 2, ¶2 on page 913 of this reference, attached). Applicants note that "[a] patent need not teach, and preferably omits, what is well known in the art." Spectra-Physics, Inc. v. Coherent, Inc., 827 F.2d 1524, 1534, 3 USPQ2d 1737, 1743 (Fed. Cir. 1987). "The forced recitation of known sequences in patent disclosures would only add unnecessary bulk to the specification. Accordingly we hold that where, as in this case, accessible literature sources clearly provided, as of the relevant date, genes and their nucleotide sequences (here 'essential genes'), satisfaction of the written description requirement does not require either the recitation or incorporation by reference ... (where permitted) of such genes and sequences" In Falker-Gunter Falkner et al. v. Inglis et al. (Fed. Cir. 2006, 05-1324, p. 17).

Item 9. 37 C.F.R. §1.75(c)

Applicants believe the rejection is overcome by the amendment of claim 1.

Applicants note that dependent claims 2, 3 and 11 cannot be broader than Claim 1, from which they depend, since the sequences encompassed by these dependent claims must also hybridize to the complement of SEQ ID NO: 3 under the conditions spelled out in claim 1. Thus, the claim elements in claims 2, 3 and 11 limit, rather than broaden, these dependent claims.

In light of these amendments, Applicants request that the objection under 37 C.F.R. §1.75(c) be withdrawn.

Item 12. 35 U.S.C. §112, first paragraph, written description

Applicants believe that the rejection under 35 U.S.C. §112, first paragraph, for lack of an adequate written description, has been in part avoided by the amendment of the claims. Other aspects of this rejection are respectfully traversed. Specific points raised in the Office action are presented in boldface. Applicants' responses are presented below each of the excerpts from the Office action.

> **The specification also does not describe nucleotide sequences encoding a genus of polypeptides having a conserved domain with at least 83% sequence identity to the conserved domain of amino acid coordinates 26-116 of SEQ ID NO:4. The specification further does not describe the nature or extent of the structural or functional homology between the disclosed sequences of SEQ ID NOS: 3 and 4 and the orthologs and homologs identified in databases.**

As shown in Table 6 on page 95 of the present application, *Arabidopsis* sequences G482, G481, G485 and rice sequence G3395 (SEQ ID NOs: 2, 4, 6 and 74, respectively) each have the ability to confer increased tolerance to at least some of various abiotic stresses, including heat, drought, salt, sugar, ABA and cold. G481 and G3395 both have conserved B domains that are 83% identical to the similar domain of G482. G485 has a B domain with an intermediate identity, 94%, to the G482 domain (see Table 1 beginning on page 31). Thus, the specification describes two nucleotide sequences that encode polypeptides having conserved domains with at least 83% sequence identity to the conserved domain of amino acid coordinates 26-116 of SEQ ID NO: 4, and, furthermore, these sequences function in transgenic plants as claimed.

The specification also provides methods for identifying orthologs and homologs using percentage identity and hybridization methods, both well recognized arts. For example, "[t]he transcription factors of the present invention each possess a B or conserved domain, including the orthologs of G482 found by BLAST analysis, as described below" (page 33, lines 1-2). See also page 37, line 11 through page 38, line 4. Hybridization conditions provided in the specification are also note above in support of the claims amendments. G3395, for example, is a sequence found in a sequence database, determined to be similar to G482 and its function paralogs, and successfully tested in plants.

> **In addition, the specification fails to provide sufficient antecedent basis for the limitations in claims 2 and 3; "Asn-$(Xaa)_4$-Lys-$(Xaa)_{33-34}$-Asn-Gly" at claim 2 and "Ser-$(Xaa)_9$-Asn-$(Xaa)_4$-Lys-$(Xaa)_{33-34}$-Asn-Gly" at claim 3. The specification at page 29 describes specific amino acids to which Claims 2 and 3 recite any amino acid would be sufficient.**
>
> **Hence, it is unclear that Applicant was in possession of the invention as broadly claimed.**

Antecedent basis in the specification for "Asn-$(Xaa)_4$-Lys-$(Xaa)_{33-34}$-Asn-Gly" is provided on page 29, line 33: Antecedent basis in the specification for "Ser-$(Xaa)_9$-Asn-$(Xaa)_4$-Lys-$(Xaa)_{33-34}$-Asn-Gly" is provided in the specification at page 30, line 4. As noted in the specification on page 29, "As can be seen in [and hence determined by alignments such as found in] Figure 6B-6C, the B domain of the non-LEC1-like clade (identified in Figures 3 and 4) may be distinguished by [these] amino acid residues".

The Federal Circuit has recently clarified the application of the written description requirement. The court stated that "A description of a genus of cDNAs may be achieved by means of recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." See University of California v. Eli Lilly and Co., 119 F.3d 1559, 1569; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). The court has also affirmed the PTO's applicable standard for determining compliance with the written description requirement, quoting from the PTO's Guidelines for Examination of Patent Applications Under the 35 U.S.C. 112, P1, "Written Description" Requirement, 66 Fed. Reg. 1099, 1106, where it is set forth that the written description requirement can be met by "show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics ._¬i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics." See Enzo Biochem Inc. v. Gen-Probe Inc., 63 USPQ2d 1609, 1613 (CAFC 2002).

Applicants did indeed provide "a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus". See, for example, the list of conserved B domains found in Table 1 beginning at page 31.

The Lilly court set out exemplary ways in which a genus of cDNAs could be described: "[a] description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, *defined by nucleotide sequence*, falling within the scope of the genus", 296 F.3d, 63 USPQ2d, *emphasis* added. The number of functional sequences described represent a practical sampling of a considerable number of sequence species. Between the eudicots soy and *Arabidopsis*, and the monocot rice, are a very large number of plant species and their related sequences. There are about 170,000 eudicot plant species that can produce G482 homologs evolutionarily more closely related to SEQ ID NOs: 3-4 than to the rice G3395 ortholog. These functionally related sequences found in very diverse plant species strongly suggest that a considerable majority, if not all or almost all, of the plant species between *Arabidopsis* and rice will have conserved G482 homolog structure and associated function. To suggest otherwise would be to suggest that very similar sequences in distantly related plant species exist because of mere coincidence and not the evolutionary imperative to retain sequence structure and function. Many orthologous monocot-derived sequences (there are about 65,000 monocot species) should also retain similar functions; it seems unlikely that rice, the first species examined and found to have a structurally and functionally related sequence, is the only monocot plant to have retained functional an orthologous G482 clade transcription factor after 130 to 240 million years of evolution (the generally accepted span from the monocot-eudicot divergence).

The Office action contends that the da Costa e Silva reference confirms "a method of producing transgenic plants tolerant to [water deprivation]. The sequences used by da Costa e Silva were derived from a moss, a very primitive plant and distant (from *Arabidopsis* or rice) plant. Thus, the Examiner's assertion would seem to support the definitive conservation of structure and function and the very high likelihood of finding with routine experimentation numerous sequences from very diverse species that function as claimed.

Thus, the skilled artisan would understand that a very large number of sequences encompassed by the claims can be readily found in plant species that lie in intermediate positions on the evolutionary tree, and would recognize that Applicants described and were in possession of many examples of functional species each comprising *partial structures coupled with a disclosed correlation between function and structure* (Enzo, *supra*) common to members of the genus.

Furthermore, the presently amended claims mirror "Example 9: Hybridization" of the USPTO Written Description Guidelines (attached). This example provides the claim (emphasis added):

"An isolated nucleic acid that specifically hybridizes under highly stringent conditions to the complement of the sequence set forth in SEQ ID NO: 1, wherein said nucleic acid encodes a protein that binds to a dopamine receptor and stimulates adenylate cyclase activity".

A single species is disclosed, a specific activity is thus recited, there is actual reduction to practice, and the highly stringent hybridization conditions are disclosed as "6XSSC and 65 degrees Celsius".

Contrast this example claim with presently amended claim 1 (emphasis added):

"A transgenic plant comprising a recombinant polynucleotide encoding a polypeptide having a conserved domain, wherein:

the recombinant polynucleotide specifically hybridizes to the complement of the sequence set forth in SEQ ID NO: 3 under stringent conditions comprising two wash steps of 1x SSC, 1% SDS at 60° C for 45-60 minutes for each wash step; and

the polypeptide binds to a transcription regulating region comprising the motif CCAAT and has the property of SEQ ID NO: 4 of regulating abiotic stress tolerance in a plant when the polypeptide is overexpressed;

wherein said binding confers increased abiotic stress tolerance in said transgenic plant as compared to a non-transformed plant that does not overexpress the polypeptide, and

wherein the increased abiotic stress tolerance is selected from the group consisting of increased tolerance to cold, increased tolerance to salt, increased tolerance to mannitol, and increased tolerance to water deprivation.

Rather than claiming "highly stringent hybridization conditions", instant claim 1 spells out precise hybridization conditions that are likely to be more stringent (1X SSC at 60 C vs. 6X SSC at 65 C) that those

found in Example 9 of the Guidelines. And, in contrast to Example 9, four, rather than one, functional species are disclosed, and numerous putative orthologs are provided (see, for example, Figures 6A-6F).

Thus, the present independent claims provide better support and are almost certainly narrower in scope, based on the specified hybridization conditions, than the example provided in the Guidelines.

In light of these amendments, arguments and experimental observations confirming Applicants' disclosure and claims, Applicants request that the rejection under 35 U.S.C. §112, first paragraph, for lack of written description, be withdrawn.

Item 12. 35 U.S.C. §112, first paragraph, enablement

The rejection under 35 U.S.C. §112, first paragraph, for being non-enabling, is respectfully traversed. Specific points raised in the Office action are presented in boldface. Applicants' responses are presented below each of the excerpts from the Office action.

Table 6 on page 95 of the specification ... teaches varying phenotypes of the transformed plants, for example G482 gave heat tolerance but not drought tolerance, but G481 did not give heat tolerance but did give drought tolerance.

Table 6, in fact, does not necessarily show varying phenotypes, but does show phenotypes that were observed with a limited number of lines that were generated to support the claims. Absence of a positive result thus does not mean that the sequence fails to provide the trait, but merely that the trait has not been observed thus far. For example, G481 did confer hyperosmotic stress tolerance, as shown in priority application 60/166,228, which is a strong indication that the sequence will also confer drought tolerance, another form of hyperosmotic stress. And, in fact, subsequent experiments with a greater number of transgenic plant lines have shown that G481 does confer drought tolerance in plants. See, for example, priority US patent application 10/374,780, Table 4 on page 67: "[SEQ ID NO:] 87 ...G481..OE [overexpressor] ...Drought...Increased tolerance to drought". For reasons noted herein, Applicants believe that many sequences that fall within the scope of the claims, for example, sequences listed in Table 1, will function as claimed by conferring increased tolerance to water deprivation, salt, cold, etc.

The specification also does not teach nucleotide sequences encoding a genus of polypeptides having a conserved domain with at least 83% sequence identity to the conserved domain of amino acid coordinates 26-116 of SEQ ID NO:4. The specification further does not teach the nature or extent of the structural or functional homology between the disclosed sequences of SEQ ID NOS: 3 and 4 and the orthologs and homologs identified in databases.

As indicated above, Table 6 on page 95 discloses that *Arabidopsis* sequences G482, G481, G485 and rice sequence G3395 (SEQ ID NOs: 2, 4, 6 and 74, respectively) each have the ability to confer increased tolerance to at least some of various abiotic stresses, including heat, drought, salt, sugar, ABA and cold. G481 and G3395 both have conserved B domains that are 83% identical to the similar domain of G482. G485 has a

B domain with an intermediate identity (94%) to the G482 domain (see Table 1 beginning on page 31). Thus, the specification does indeed describe nucleotide sequences encoding a genus of polypeptides having a conserved domain with at least 83% sequence identity to the conserved domain of amino acid coordinates 26-116 of SEQ ID NO:4, and, furthermore, these sequences function in transgenic plants as claimed.

Table 1 of the specification also provides numerous sequences that are homologous to SEQ ID NO: 3-4 and below Table 1 it is disclosed that "[t]he transcription factors of the present invention each possess a B or conserved domain, including the orthologs of G482 found by BLAST analysis, as described below. Generally, the B domain of the transcription factors will bind to a transcription-regulating region comprising the motif CCAAT" (page 32, lines 1-5, emphasis added) "Orthologs and paralogs are evolutionarily related genes that have similar sequence and similar functions" (page 37, lines 7-8, emphasis added). Table 1 thus includes prophetic examples ("[a]n example may be 'working' or 'prophetic' ", MPEP 2164.02").

The specification also provides methods for identifying orthologs and homologs using percentage identity and hybridization methods, both well recognized arts. For example, "[t]he transcription factors of the present invention each possess a B or conserved domain, including the orthologs of G482 found by BLAST analysis, as described below" (page 33, lines 1-2). See also page 37, line 11 through page 38, line 4. Hybridization conditions provided in the specification are also note above in support of the claims amendments. G3395, for example, is a sequence found in a sequence database, determined to be similar to G482 and its function paralogs, and successfully tested in plants.

> **The full scope of the claimed invention is not enabled because it is unpredictable whether a variant of SEQ ID NOS: 3 or 4 would encode a polypeptide that increases the transgenic plant's tolerance to stress. It is unpredictable because specific protein function requires the presence of particular amino acid residues in specific locations, which particular amino acid residues may not be retained by a variant.**

Contrary to this assertion, Applicants have shown that sequences homologous to SEQ ID NOs: 3 and 4 from very diverse species predictably confer the phenotype of increased tolerance to numerous abiotic stresses (e.g., as noted in Table 6). Regarding the Wands factors, Applicants wish to note that it would not require undue experimentation to find sequences that are closely-related to G482 using BLAST or hybridization analysis, test them in plants, and identify those sequences that confer increased tolerance to the claimed abiotic stresses. In fact, as noted above, since sequences from both dicots and monocots confer increased abiotic stress, the likelihood of finding other operative species is high since conservation of structure and function has been conserved over many millions of years and in thousands of plant species. See, also, the da Costa e Silva reference cited in the Office action which allegedly confirms "a method of producing transgenic plants tolerant to [water deprivation]. The sequences used by da Costa e Silva were derived from a moss. Thus, the Office action seems to support the high conservation of structure and function and the very high likelihood of finding, with routine experimentation, numerous sequences from very diverse species that function as claimed.

Smolen et al., (Genetics, 2002, Vol. 161, pages 1235-1246) ...teach that an aspartate to asparagine change in a highly conserved position in the N-terminal region of the RIB basic helix loop plant transcription factor ATR2 causes increased expression of several tryptophan genes as well as a subset of other stress responsive genes in mutant plants expressing the variant sequence as compared to wild-type plants expressing the wild type sequence (page 1238 Figure 2). Smolen et al. also teach that transgenic plants overexpressing the variant sequence exhibit increased purple pigmentation, reduced size, and reduced fertility as compared to transgenic plants that overexpress the wild type sequence (paragraph spanning pages 11235-1240 and Figure 3)....

in the instant case Applicant has not provided sufficient guidance with respect to which variants of SEQ ID NOS: 3 or 4 would retain the necessary amino acid residues such that the variant encodes a polypeptide that increases the transgenic plant's tolerance to environmental stresses as broadly claimed. Absent such guidance one skilled in the art would have to make and test each subsequence or fragment or variant in order to discriminate between those protein variants that would be useful for preparing a transgenic plant having increased tolerance to stress and those that would not. Such a trial and error experimental approach would constitute undue experimentation.

Applicants are unsure how the Smolen reference relates to the present claims. The fact that some changes in functional residues in any protein can produce unpredictable results is not at issue. The present claims require the functions of increased abiotic stress tolerance. While it may be possible to create a non-functional species of practically any invention (e.g., proteins can be denatured or physically isolated from their targets), the possible existence of non-functional species is not at issue; "[w]ithout undue experimentation or effort or expense the combinations which do not work will readily be discovered and, of course, nobody will use them and the claims do not cover them", *In re Angstadt*, 537 F.2d at 504, 190 USPQ at 219. Furthermore, is not a function of the claims to specifically exclude . . .possible inoperative substances . . ." *In re Dinh-Nguyen*, 492 F.2d 856, 858-59, 181 USPQ 46, 48 (CCPA 1974) (emphasis omitted). Accord, *In re Geerdes*, 491 F.2d 1260, 1265, 180 USPQ 789, 793 (CCPA 1974); *In re Anderson*, 471 F.2d 1237, 1242, 176 USPQ 331, 334-35 (CCPA 1973). "[T]ypically, inoperative embodiments are excluded by language in a claim" (MPEP 2164.08(b)). If a plant is transformed with, for example, a transcription factor structurally related to a sequence of the invention but does not act as a transcription factor and/or does not increase tolerance to the claimed abiotic stresses, such a plant would not meet the requirement of the claims. Contrarily, as Applicants have shown, it is a matter of routine to find sequences that are encompassed by the claims and function as claimed.

The full scope of the claimed invention is also not enabled because the ability of a plant transcription factor coding sequence to increase tolerance to different types of stresses is unpredictable. It is unpredictable because the activity of different combinations of genes is required for tolerance to a particular type of stress, such that the ability of a transcription factor polypeptide to increase tolerance to a particular type of stress depends on the extent to which that transcription factor polypeptide activates the expression of the genes whose activity is required for tolerance to that stress.

See, for example, Liu et al. (The Plant Cell, 1998, Vol. 10, pages 1391-1406), who teach that two transcription factors, DREB1 and DREB2, function in two separate signal transduction pathways under low temperature and dehydration conditions respectively. The expression of DREB1 transcription factors is induced by low temperature stress, whereas the expression of DREB2 transcription factors is induced by dehydration and high-salt stress (page 1398 Figure 6). Furthermore, over-expression of DREB1 in transgenic plants induced the expression of rd29A, a gene whose expression is induced by dehydration, high salt and low temperature stress in non-transgenic wild type plants, whereas over-expression of DREB2 did not induce rd29A expression (page 1402 Figure 11).

As noted above, G482 homologous sequences from very diverse plant species have been shown to function as claimed by conferring increased tolerance to the claimed abiotic stresses. This apparently includes sequence derived from a primitive moss species, as suggested in the Office action citing the da Costa e Silva reference. Thus, the ability of the plant transcription factor coding sequences being claimed to increase tolerance to different types of stresses is highly conserved and therefore quite predictable.

Regarding the Liu reference, "plants have common mechanisms in their physiological responses and tolerance to drought and low temperature" (p. 1391, col. 1, paragraph 1). Thus, there are many aspects of cold, drought and salt stress responses that act in common, and the responses to low temperature and dehydration conditions share common pathway components. Liu et al. note that "DREB1 and DREB2, bind to the same target sequence, DRE, and are involved in the activation of the rd29A gene in response to dehydration, high-salt, and low-temperature stress (page 1399, col. 1, paragraph 1)" Thus, "[b]ased on the commonality of many aspects of cold, drought and salt stress responses, it can be concluded that genes that increase[d] tolerance to cold or salt stress can also improve drought stress protection" (present specification, page 6, lines 8-13).

> **In the instant case Applicant has not provided sufficient guidance with respect to which types of environmental stress tolerance would be conferred to plants the express the plant transcription factor coding sequences recited in the claims. ..one skilled in the art would have to test transgenic plants comprising each plant transcription factor coding sequence under a variety of different conditions in order to discriminate between stress conditions the transgenic plants would tolerate and stress conditions they would not tolerate. Such a trial and error experimental approach would constitute undue experimentation.**

Claim 1 comprises the claim element "abiotic stress tolerance ... selected from the group consisting of increased tolerance to cold, increased tolerance to salt, increased tolerance to mannitol, and increased tolerance to water deprivation." Claim 12 comprises the claim element "abiotic stress ... selected from the group consisting cold, salt, mannitol, and water deprivation". There is thus very specific guidance with respect to which types of environmental stress tolerance would be conferred to plants that express the plant transcription factor coding sequences recited in the claims.

The Office action does not state why testing transgenic plants comprising plant transcription factor coding sequences under a variety of different conditions would constitute a trial and error approach. In fact, this approach is exactly the sort of routine experimentation in which Applicants engage, and it is apparently the sort of approach, according to the Office action, engaged in by da Costa e Silva. Since very diverse plant species have retained very similar sequences that confer the function of increasing tolerance to the claimed abiotic stresses, it is a matter of routine to find functional sequences from the numerous plants that fall, for example, between eudicots and monocots, or, according to the Office action, between eudicots and mosses.

In light of these amendments, arguments and experimental observations confirming Applicants' disclosure and claims, Applicants request that the rejection under 35 U.S.C. §112, first paragraph, for lack of enablement, be withdrawn.

Item 14. 35 U.S.C. §102(b)

Applicants believe the rejection under 35 U.S.C. §102 has been avoided by the present amendment. Specific points raised in the Office action are presented in boldface. Applicants' responses are presented below.

Claims 1-3, 5, 6, 10-13 and 15 are rejected under 35 U.S.C. § 102(e) as being anticipated by da Costa e Silva et al (U.S. Patent 6,677,504, filed 6 April 2001 and claiming benefit of U.S. Provisional Application 601196,001 filed 7 April 2000) taken with the evidence of Fourgoux-Nicol et a1 (1999, Plant Molecular Biology 40: 857-872).

As noted above, independent claims 1 and 12 have been amended such that the recombinant polynucleotide comprised within the transgenic plants of the invention specifically hybridizes to the complement of the sequence set forth in SEQ ID NO: 3 under stringent conditions comprising two wash steps of 1x SSC, 1% SDS at 60° C for 45-60 minutes for each wash step. SEQ ID NO: 3 and this hybridization language may be found in priority application 60/166,228, filed November 17, 1999 (e.g., see the pages for "Summary of Overexpressor G482, Family CAAT", and page 20, lines 10-11). Application 60/166,228 teaches how to prepare transgenic plants, and discloses osmotic stress-tolerant transgenic plants overexpressing G481 (present SEQ ID NO: 2) and salt-tolerant transgenic plants overexpressing G482 (presently SEQ ID NO: 4). Application 60/125,814, filed March 23, 1999 discloses sequence "G482" in "Family 13. CAAT Binding Protein...", and hybridization methods and conditions on, for example, page 47, lines 1-2 and page 63, lines 25-31.

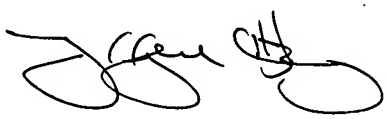
Applicants believe these and subsequent priority applications disclose the present sequences, transgenic plants, and methods for determining abiotic stress tolerance. Both of these applications were filed before the priority date of USPN 6,677,504, and priority application 60/125,814 was filed prior to the Fourgoux-Nicol et a1 reference which was "taken with the evidence of" USPN 6,677,504 for the purposes of establishing a rejection under 35 U.S.C. § 102(e).

Accordingly, Applicants request that the rejection under 35 U.S.C. §102(e) be withdrawn.

CONCLUSION

Applicants believe that no additional fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Mendel Biotechnology, Inc. Deposit Account No. **50-1025.**

Respectfully submitted,
MENDEL BIOTECHNOLOGY, INC.



Date: 11 September 2007

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JML/jml
File: MBI-0022CIP.ROA.doc

Attachments:

- Transmittal Form
- Petition for Extension of Time under 1.136(a)
- Substitute Sequence Listing in Computer Readable Form
- Transmittal of Sequence Listing under 37 C.F.R. §§1.821-1.825 and §1.821(f)
- Reference: Jaglo et al. (2001) *Plant Physiol.* 127: 910-917
- Figures 6A-6B, Replacement sheets and annotated sheets showing changes
- 4 pages from Written Description Guidelines

SEQ ID NOs: added

```
G3472 (80)          ---------------MAES-----------DNESGGHTGNASGSN-------------
G3473 (52)          ---------------MADS-----------DNDSGGAHNGGKGS--------------
G3474 (82)          ---------------MAES-----------DNESGGHTGNASGSN-------------
G3435 (48)          ---------------MPDS-----------DNDSGGPSN-AGG---------------
G3397 (92)          ---------------MPDS-----------DNDSGGPSNYAGG---------------
G3436 (50)          ---------------MPDS-----------DNESGGPSN--A-----------------
G3398 (76)          ---------------MPDS-----------DNESGGPSN--AG----------------
G3475 (20)          ---------------MADS-----------DNDSGGAHNAGKG---------------
G3478 (86)          ---------------MADS-----------DNDSGGAHNGGKG---------------
G3476 (18)          ---------------MAES-----------DNDSGGAQNAGNSGNL------------
G485   (6)          ---------------MADS-----------DNDSGGHKDGGN-----------------
G482   (4)          ---------------MGDS-----------DRDSGGGQNGNNQNGQ------------
OSC30077 (31)       MKSRKSYGHLLSPVGSPPL-----------DNESGEAAAAAAAGGGGCGSSAGYVVYGG
G3471 (24)          ---------------MSDAPPSP--------THESGGEQSPRGSS--------------
G3477 (84)          ---------------MSDAPASP--------SHESGGEQSPRGSL--------------
G3470 (26)          ---------------MSDAPASP--------SHESGGEQSPRGSL--------------
G481   (2)          ---------------MADTPSSP--------AGD-GGESG-------------------
G1364  (8)          ---------------MAESQAKSP---GGCGSHESGGDQSPR-----------------
G2345 (10)          ---------------MAESQTGG----GGGGSHESGGDQSPR-----------------
AP004366 (110)      ---------------MADA-----------GHDESGSPPRSGGVR--------------
G3434 (78)          ---------------MADD-----------GGSHEGSG-GGGGVR--------------
G3394 (88)          ---------------MADGPGSPG---GGGGSHESGSPRGGGGGGGGG------------
G1781 (72)          ---------------MTEESPEEDHGSPGVAETNPGSPSSKTNNNNN-------------
G1248 (70)          ---------------MAGNYHSFQNPIPRYQNYNFGSSSSNHQHEHDGLVV----VVEDQ
G486  (111)         ------------------------------------------------------------
G1821 (112)         ---------------MAEGSMRPP-------EFNQPNKTSNGGEE--------------
Consensus (113)                     M D                   GG
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FIGURE 6A

SEQ ID NOs: added

DNA binding domain

Subunit interaction

```
G3472 (80)          ---EFSGCREQDRFLPIANVSRIMKKALPANAKISKEAKETVQECVSEFISFIT-GEASD
G3473 (52)          ---EMS-PREQDRFLPIANVSRIMKKALPANAKISKDAKETVQECVSEFISFHSPGGLAG
G3474 (82)          ---ELSGCREQDRFLPIANVSRIMKKALPANAKISKEAKETVQECVSEFISFIT-GEASD
G3435 (48)          ---ELSSPREQDRFLPIANVSRIMKKALPANAKISKDAKETVQECVSEFISFIT-GEASD
G3397 (92)          ---ELSSPREQDRFLPIANVSRIMKKALPANAKISKDAKETVQECVSEFISFIT-GEASD
G3436 (50)          ---EFSSPREQDRFLPIANVSRIMKKALPANAKISKDAKETVQECVSEFISFIT-GEASD
G3398 (76)          ---EYASAREQDRFLPIANVSRIMKRALPANAKISKDAKETVQECVSEFISFIT-GEASD
G3475 (20)          ---SEMSPREQDRFLPIANVSRIMKKALPANAKISKDAKETVQECVSEFISFIT-GEASD
G3478 (86)          ---SEMSPREQDRFLPIANVSRIMKKALPANAKISKDAKETVQECVSEFISFIT-GEASD
G3476 (18)          ---SELSPREQDRFLPIANVSRIMKKALPANAKISKDAKETVQECVSEFISFIT-GEASD
G485   (6)          -----ASTREQDRFLPIANVSRIMKKALPANAKISKDAKETVQECVSEFISFIT-GEASD
G482   (4)          ---SSLSPREQDRFLPIANVSRIMKKALPANAKISKDAKETMQECVSEFISFVT-GEASD
OSC30077 (31)       GGGGDSPAKEQDRFLPIANVSRIMKRSLPANAKISKESKETVQECVSEFISFVT-GEASD
G3471 (24)          ----SG-AREQDRYLPIANISRIMKKALPPNGKIAKDAKDTMQECVSEFISFIT-SEASE
G3477 (84)          ----SGAAREQDRYLPIANISRIMKKALPPNGKIAKDAKDTMQECVSEFISFIT-SEASE
G3470 (26)          ----SGAAREQDRYLPIANISRIMKKALPPNGKIAKDAKDTMQECVSEFISFIT-SEASE
G481   (2)          -----GSVREQDRYLPIANISRIMKKALPPNGKIGKDAKDTVQECVSEFISFIT-SEASD
G1364  (8)          ----SLHVREQDRFLPIANISRIMKRGLPANGKIAKDAKEIVQECVSEFISFVT-SEASD
G2345 (10)          ----SLNVREQDRFLPIANISRIMKRGLPLNGKIAKDAKETMQECVSEFISFVT-SEASD
AP004366 (110)      ---------EQDRFLPIANISRIMKKAVPANGKIAKDAKETLQECVSEFISFVT-SEASD
G3434 (78)          ---------EQDRFLPIANISRIMKKAVPANGKIAKDAKETLQECVSEFISFVT-SEASD
G3394 (88)          --GGGGPLVRQDRFLPIANISRIMKKAIPANGKIAKDAKETVQECVSEFISFIT-SEASD
G1781 (72)          ------NNKEQDRFLPIANVGRIMKKVLPGNGKISKDAKETVQECVSEFISFVT-GEASD
G1248 (70)          QQEESMMVKEQDRLLPIANVGRIMKNILPANAKVSKEAKETMQECVSEFISFVT-GEASD
G486  (111)         -------MTDEDRLLPIANVGRLMKQILPSNAKISKEAKQTVQECATEFISFVT-CEASE
G1821 (112)         ----ECTVREQDRFMPIANVIRIMRRILPAHAKISDDSKETIQECVSEYISFIT-GEANE
Consensus (113)           EQDRFLPIANVSRIMK ALPANAKISKDAKETVQECVSEFISFIT GEASD
```

B domain

FIGURE 6B

SEQ ID NOs: added

```
G3472 (80)        KCQKEKRKTINGDDLLWAMTTLGFEEYVEPLKVYLHKYRELEGEKTAMMG----------
G3473 (52)        ECQKEKRKTINGDDLLWAMTTLGFEEYVEPLKVYLHKYRELEGEKTAMMG----------
G3474 (82)        KCQKEKRKTINGDDLLWAMTTLGFEDYVDPLKIYLHKYREMEGEKTAMMG----------
G3435 (48)        KCQREKRKTINGDDLLWAMTTLGFEDYVEPLKHYLHKFREIEGERAAASAGASGSQQQ--
G3397 (92)        KCQREKRKTINGDDLLWAMTTLGFEDYVDPLKHYLHKFREIEGERAAASTTGAGTSAA--
G3436 (50)        KCQREKRKTINGDDLLWAMTTLGFEDYVEPLKLYLHKFRELEGEKAATTSASSGPQPPLH
G3398 (76)        KCQREKRKTINGDDLLWAMTTLGFEDYIDPLKLYLHKFRELEGEKAIGAAGSGGGGAASS
G3475 (20)        KCQREKRKTINGDDLLWAMTTLGFEDYVEPLKGYLQRFREMEGEKTVAAR----------
G3478 (86)        KCQREKRKTINGDDLLWAMTTLGFEDYVEPLKGYLQRFREMEGEKTVAAR----------
G3476 (18)        KCQREKRKTINGDDLLWAMTTLGFEEYVEPLKIYLQRFREMEGEKTVAAR----------
G485   (6)        KCQREKRKTINGDDLLWAMTTLGFEDYVEPLKVYLQKYREVEGEKTTTAGR---------
G482   (4)        KCQKEKRKTINGDDLLWAMTTLGFEDYVEPLKVYLQRFREIEGERTGLGRP---------
OSC30077 (31)     KCQREKRKTINGDDLLWAMTTLGFEAYVGPLKSYLNRYREAEGEKADVLGGAGGAAAARH
G3471 (24)        KCQKEKRKTINGDDLLWAMATLGFEDYIEPLKVYLARYREAEGDTKGSARS---------
G3477 (84)        KCQKEKRKTINGDDLLWAMATLGFEDYIEPLKVYLARYREAEGDTKGSARS---------
G3470 (26)        KCQKEKRKTINGDDLLWAMATLGFEDYIEPLKVYLARYREAEGDTKGSARS---------
G481   (2)        KCQKEKRKTVNGDDLLWAMATLGFEDYLEPLKIYLARYRELEGDNKGSGKS---------
G1364  (8)        KCQREKRKTINGDDLLWAMATLGFEDYMEPLKVYLMRYRE--GDTKGSAKG---------
G2345 (10)        KCQREKRKTINGDDLLWAMATLGFEDYIDPLKVYLMRYREMEGDTKGSGKG---------
AP004366 (110)    KCQKEKRKTINGEDLLFAMGTLGFEEYVDPLKIYLHKYREMEGDSKLSSKA---------
G3434 (78)        KCQKEKRKTINGDDLLWAMATLGFEEYVEPLKIYLQKYKEMEGDSKLSTKA---------
G3394 (88)        KCQREKRKTINGDDLLWAMATLGFEDYIEPLKVYLQKYREMEGDSKLTAKA---------
G1781 (72)        KCQREKRKTINGDDIIWAITTLGFEDYVAPLKVYLCKYRDTEGEKVNSPKQ---------
G1248 (70)        KCHKEKRKTVNGDDICWAMANLGFDDYAAQLKKYLHRYRVLEGEKPN-------------
G486  (111)       KCHRENRKTVNGDDIWWALSTLGLDNYADAVGRHLHKYREAERERTEHNKG---------
G1821 (112)       RCQREQRKTITAEDVLWAMSKLGFDDYIEPLTLYLHRYRELEGERGVSCSAG--------
Consensus (113)   KCQREKRKTINGDDLLWAMTTLGFEDY EPLKVYL  YRE EGE
```

B domain

FIGURE 6C

SEQ ID NOs: added

```
G3472 (80)       ------------RPHERDEGYGH--------------ATPMM-IMMGHQ---------
G3473 (52)       ------------RPHERDEGYGH--------------ATPMM-IMMGHQ---------
G3474 (82)       ------------RPHERDEGYGHGHG-----------HATPMMTMMMGHQPQHQHQH--
G3435 (48)       --QQQGELPRGAANAAG-YAGYGAPG-----------SG-GMMMMMMGQPMYGGSQPQ-
G3397 (92)       --STTPPQQQHTANAAGGYAGYAAPG-----------AGPGGMMMMMGQPMYGSPPP--
G3436 (50)       RETTPSSSTHN--GAGGPVGGYGMYGGA----------GGGSGMIMMMGQPMYGGSPPA-
G3398 (76)       GGSGSGSGSHHHQDASRNNGGYGMYG------------GGGGMIMMMGQPMYG-SPPA-
G3475 (20)       --DKDAPPPTNATNSAYESPSYAAA---------------PGGIMMHQGHVYG------
G3478 (86)       --DKDAPPLTNATNSAYESANYAAAA------------AVPGGIMMHQGHVYG------
G3476 (18)       --DSSK---DSASASSY-----------------------------HQGHVYG------
G485   (6)       --QGDKEGGGGGGGAGSGSGGAPMYG--------------GGMVTTMGHQFS-------
G482   (4)       --QTGGEVGEHQRDAVGDGGGFYGGG--------------GGMQYHQHHQFL-------
OSC30077 (31)    GEGGCCGGGGGGADGVVIDGHYPLAGGLSHSHHGHQQQDGGGDVGLMMGGGDAGVGYNAG
G3471 (24)       --GDGSATPD-QVGLAGQNSQLVHQG-------------SLNYIGLQVQP----------
G3477 (84)       --GDGSATPD-QVGLAGQNSQLVHQG-------------SLNYIGLQVQP----------
G3470 (26)       --GDGSARPD-QVGLAGQNAQVQPQX-------------SG--YAFNARP----------
G481   (2)       --GDGSNRDA-GGGVSGEEMPSW-----------------------------------
G1364  (8)       --GDPNAKKDGQSSQNGQFSQLAHQG-----------------PYGNSQ----------
G2345 (10)       --GESSAKRDGQPSQVSQFSQVPQQG-------------SFSQGPYGNSQSLRFGNSIEH
AP004366 (110)   --GDGSVKKDTIGPHSGASSSSAQG--------------MVGAYTQGMGY----------
G3434 (78)       --GEGSVKKDAISPHGGTSSSSNQLV-------------QHGVYNQGMGY----------
G3394 (88)       --GDGSVKKDVLGSHGGSSSSAQGMG-------------QQAAYNQGMGY----------
G1781 (72)       --QQQRQQQQQIQQQNHHNYQFQEQDQNNNN-------MSCTSYISHHHPSPFLPVDHQ-
G1248 (70)       ------------------------------------------HHGKG---------
G486  (111)      --SNDSGNEKE-------------------------------TNTRS---------
G1821 (112)      --SVSMTNGLVVKRPNGTMTEYGAYG---------------PVPGIHMAQYHYR------
```

FIGURE 6D

SEQ ID NOs: added

```
G3472 (80)       ------------QQQHQG--HVYGSGTT-------TGSASSARTR-------------
G3473 (52)       ------------QQQHQG--HVYGSGTT-------TGSASSARTR-------------
G3474 (82)       -----------QHQHQHQG--HVYGS-----------GSASSARTR-------------
G3435 (48)       --QQPPQPQPPQQQQQQHQQHHMAMGGRGGFGQQ--GGGGGSSSSSGLGRQDRA------
G3397 (92)       ---------PPQQQQQQH--HHMAMGGRGGFGHHPGGGGGGSSSSSGHGRQNRGA-----
G3436 (50)       --ASSG-------SYPHH---QMAMGGKGGAYGYGGGSSSSPS---GLGR----------
G3398 (76)       --SSAGYAQPPPPHHHHH---QMVMGGKG-AYGHGGGGGGGPSPSSGYGRQDRL------
G3475 (20)       ------------SAGFH---QVAGGAIK-------GGPVYPGPGSNAGRPR--------
G3478 (86)       ------------SAGFH---QVAGGAIK-------GGPAYPGPGSNAGRPR--------
G3476 (18)       ------------SPAYH---HQVP-----------GPTYPAPG----RPR--------
G485   (6)       ------------HHFS-----------------------------------------
G482   (4)       ------------HQQNHMYGATGGGSDS-------GGGAASGRTRT------------
OSC30077 (31)    AGSTTTAFYAPAATAASGNKAYCGGDGSRVMEFEGIGGEEESGGGGGGGERGFAGHLHGV
G3471 (24)       ----------------QHLVMPSMQSHE-------------------------------
G3477 (84)       ----------------QHLVMPSMQSHE-------------------------------
G3470 (26)       ----------------------------------------------------------
G481   (2)       ----------------------------------------------------------
G1364  (8)       -----------------VTFPLFSSHSSN-----------THH--SLLIC---------
G2345 (10)       LEVLMSSTRTLFITIFRDSTMPVVSENLSDPLSIDMDCEAIYHHFIGLLILSCK------
AP004366 (110)   --------------------MQPQSNFHILVVLQSFAFPYMYQVAQIYCKYPSIE-----
G3434 (78)       --------------------MQPQ-----------------YHNGET------------
G3394 (88)       --------------------MQPQ-----------------YHNGDVSN----------
G1781 (72)       -------------PFPNIAFSPKSLQKQ--------FPQQHDNNIDSIHW---------
G1248 (70)       ---------------------GPKSSP---------------DN---------------
G486  (111)      ---------------------DVQNQSTK--------FIRVVEKGSSSSAR---------
G1821 (112)      -----------------HQNGFVFSGNEPNSKMSGSSSGASGARVEVFPTQQHKY-----
```

FIGURE 6E

SEQ ID NOs: added

G3472	(80)	----------
G3473	(52)	----------
G3474	(82)	----------
G3435	(48)	----------
G3397	(92)	----------
G3436	(50)	----------
G3398	(76)	----------
G3475	(20)	----------
G3478	(86)	----------
G3476	(18)	----------
G485	(6)	----------
G482	(4)	----------
OSC30077	(31)	QWFRLKRNTN
G3471	(24)	----------
G3477	(84)	----------
G3470	(26)	----------
G481	(2)	----------
G1364	(8)	----------
G2345	(10)	----------
AP004366	(110)	----------
G3434	(78)	----------
G3394	(88)	----------
G1781	(72)	----------
G1248	(70)	----------
G486	(111)	----------
G1821	(112)	----------

FIGURE 6F